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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/879,312

DATE: 12/26/2001
 TIME: 10:53:17

Input Set : N:\CrF3\RULE60\09879312.txt
 Output Set: N:\CRF3\12262001\I879312.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Glimcher, Laurie H. et al.
- (ii) TITLE OF INVENTION: Human c-Mat Compositions and Methods of Use Thereof
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/879,312
 C--> 28 (B) FILING DATE: 12-Jun-2001

- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/086,010
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kara, Catherine J.
 - (B) REGISTRATION NUMBER: 41,106
 - (C) REFERENCE/DOCKET NUMBER: HUI-027CP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)742-4214

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

63	ATG GCA TCA GAA CTG GCA ATG AGC AAC TCC GAC CTG CCC ACC AGT CCC	48
64	Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro	
65	1 5 10 15	
67	CTG GCC ATG GAA TAT GTT AAT GAC TTC GAT CTG ATG AAG TTT GAA GTG	96

RAW SEQUENCE LISTING

PATENT APPLICATION NO. US/09/879,312

DATE = 12/26/01

TIME = 1:58:41

Input File = N:\Crif3\RULE60\09879312.txt

Output File = N:\CRF3\12262001\I879312.raw

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68 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
69          20          40          60          80
71 AAA AAG GAA CCG GGG GAG AGC GAG CAG AAT AAT AAT CAG TCG GGC CCG      144
72 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
73          35          40          45
75 CTC ATC GCC GGG GGC TCG CCG TCG TCG ACC CCG ATG AGC AGC CCG TCG      192
76 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
77          50          55          60
79 AGC TCG GGG CCG CCG TCG CCG AGC TCG TCG GCG CCG AGC CCG GGC TCG      240
80 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
81          65          70          75          80
83 CGA GGC GAA CAG AAG GCG CAC CCG GAA GAC TAC TAC TCG ATG ACC GGC      288
84 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
85          85          90          95
87 TAC CCG CAG CAG CCG AAC CCG GAG GCG CCG GGC TTC AGC CCG GAG GAC      336
88 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
89          100          105          110
91 GCG GTC GAG GCG CTC ATC AGC AAC AGC CAC CAG CTC CCG GGC GGC TTC      384
92 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
93          115          120          125
95 GAT GGC TAT GCG CCG GGG GCG CAG CAG CTA GCC GCG GCG GCC GGG GCA      432
96 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Gly Ala
97          130          135          140
99 GGT GCC GGC GCC TCG TCG GGC AGC GGC GAG GAG ATG GGC CCG GCC      480
100 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
101          145          150          155          160
103 GCC GCC GTG GTG TCG GCC GCG ATC GCC GCG GCC GCC GCG CAG AGC GGC      528
104 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly
105          165          170          175
107 GCG GGC CCG CAC TAC CAC CAC CAC CAC CAC CAC GCC GCC GGC CAC CAC      576
108 Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His
109          180          185          190
111 CAC CAC CCG ACG GCC GGC GCG CCG GGC GCC GCG GGC AGC GCG GCC GGT      624
112 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
113          195          200          205
115 TCG GCC GGT GGC GGT GGG GGC GCG GGC GGC GGT GGC CCG GCC AGC GTT      672
116 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Gly Pro Ala Ser Val
117          210          215          220
119 GGG GGC GGC GGC GGC GGC GGC GGC GGA GGC GGC GGG GGC GCG GCG      720
120 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
121          225          230          235          240
123 GGC GCC CTG CAC CCG CAC CAC GCC GCC GGC GGC CTG CAC TTC GAC GAC      768
124 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
125          245          250          255
127 CGC TTC TCC GAC GAG CAG CTG GTG ACC ATG TCT GTG CGC GAC TGG AAC      816
128 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
129          260          265          270
131 CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CCG CTG AAG CAG      864
132 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/879,312

DATE: 01/26/2004

TIME: 11:45:21

SEQUENCE: N:\CrF3\RU1E60\09879312.Lxl

SEQUENCE: N:\CRF3\12262001\1879312.raw

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135          175          215          255          295          335          375          415          455          495
135 AAG AGG CGG AGG TGG AAA AAC CGC GGC TAT GGT AAG TCC TGC CGG TTT          912
136 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
137          200          240          280          320          360          400          440          480          520          560
139 AAG AGG GGG CAG CAG AGA CAC GTC CCG CAG TCG TAG AAG AAC TAT TGG          960
140 Lys Arg Val Gln Gln Arg His Val Leu Gln Ser Gln Lys Asn Gln Leu
141 305          340          380          420          460          500          540          580          620          660
143 CIG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CIG GIG CCG          1008
144 Leu Gln Gln Val Asn His Leu Lys Gln Gln Ile Ser Arg Leu Val Arg
145          325          360          400          440          480          520          560          600          640          680
147 GAG AGG GAC GGC TAC AAG CAG AAA TAC GAG AAG TTG GIG AGC AGC GGC          1056
148 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
149          340          380          420          460          500          540          580          620          660          700
151 TTC CGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCC TCT CCC GAG TTT          1104
152 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
153          355          400          440          480          520          560          600          640          680          720
155 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC          1152
156 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
157          370          410          450          490          530          570          610          650          690          730
159 ACA TTT TGG AAG CCC CAG CAT CGI GGA CTT ACC AGT GIG TTC ACA AAA          1200
160 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
161 385          390          395          400
163 TGA          1203
168 (2) INFORMATION FOR SEQ ID NO: 2:
170 (i) SEQUENCE CHARACTERISTICS:
171 (A) LENGTH: 400 amino acids
172 (B) TYPE: amino acid
173 (D) TOPOLOGY: linear
175 (ii) MOLECULE TYPE: protein
177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
179 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
180 1 5 10 15
182 Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
183 20 25 30
185 Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
186 35 40 45
188 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
189 50 55 60
191 Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
192 65 70 75 80
194 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
195 85 90 95
197 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
198 100 105 110
200 Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
201 115 120 125
203 Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
204 130 135 140
206 Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala

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RAW SEQUENCE LISTING

US/09/879,312

DATE: 12/26/2001

TIME: 15:33:27

File Path: N:\Crif3\RUIF60\09879312.txt

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237 241
238 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly
240 165 170 175
242 Ala Gly Pro His Leu His His His His His His Ala Ala Gly His His
243 180 185 190
245 His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala
246 195 200 205
248 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Pro Ala Ser Val
249 210 215 220
251 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
252 225 230 235 240
254 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
255 245 250 255
257 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
258 260 265 270
280 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
281 275 280 285
283 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
284 290 295 300
286 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
287 305 310 315 320
289 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
290 325 330 335
292 Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
293 340 345 350
295 Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe
296 355 360 365
298 Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
299 370 375 380
301 Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
302 385 390 395 400

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VERIFICATION SUMMARY

FILE: FILE# 00000000 US/09/879,312

FILE: 12/26/01

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FILE: 00000000 N:\Crif3\RULE60\09879312.txt

FILE: 00000000 N:\CRF3\12262001\I879312.raw

FILE: 00000000 Forward mispelled or invalid format [(A) APPLICATION NUMBER.]
FILE: 00000000 Forward mispelled or invalid format [(B) FILING DATE.]